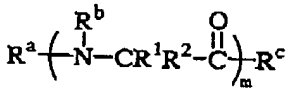
Listing of Claims:

1-12. (Canceled)

13. (Currently amended) A method of identifying peptoids which are effective in transfecting a cell with an oligonucleotide, the method comprising

(i) providing a library of peptoids in an array of physically separated compartments, said peptoids having a plurality of different sequences and having the general formula I:



I

where

R^a is selected from the group consisting of alkyl, aryl, aralkyl, aralkenyl, and aralkynyl, any of which may be substituted with one or more groups X; hydrogen, -OH, -SH, -COOH, sulfonyl, and a lipid moiety, wherein said lipid moiety may be conjugated to a linker moiety,

each R^b is independently selected from the group consisting of alkyl, aryl, aralkyl, aralkenyl, and aralkynyl, any of which may be substituted with one or more groups X; and hydrogen,

wherein at least one group R^b is not hydrogen;

R^c is selected from the group consisting of alkyl, aryl, aralkyl, aralkenyl, and aralkynyl, any of which may be substituted one or more groups X; hydrogen, -OH, -SH, $-NH_2$, -NHR, -NH(C=O)R, where R is lower alkyl; sulfonyl, hydrazine, and a lipid moiety, wherein said lipid moiety may be conjugated to a linker moiety;

X is selected from hydroxy, alkoxy, amino, guanidino, amidino, alkylamino, alkylthio, halogen, nitro, cyano, keto, aldehyde, carboxylic acid, carboxylic ester, carboxylic amide, sulfonic acid and sulfonic ester;

at least one of R^a and R^c comprises a lipid moiety;

R^1 and R^2 are independently selected from hydrogen, lower alkyl, and lower alkoxy; and

m is an integer selected from 2 to about 50, wherein

the sequences of individual peptoids in the library are unidentified;

(ii) contacting a plurality of peptoids having unidentified sequences from the library provided in (i) with an oligonucleotide, to form a plurality of peptoid-oligonucleotide mixtures, wherein said oligonucleotide is between about 10 and 50 nucleotides in length, and wherein said contacting is performed in an array of physically separated compartments;

(iii) contacting each said mixture with a cell in an array of physically separated compartments;

(iv) screening each cell for transfection of the oligonucleotide, to identify transfected cells; and

(v) identifying transfecting peptoids in mixtures contacted with transfected cells.

14. (Canceled)

15. (Currently amended) The method of claim [[14]] 13, wherein said peptoids are supported on solid particles in said physically separated compartments.

16. (Previously presented) The method of claim 15, further comprising the step of releasing the peptoids from the particles in said compartments, prior to said contacting step (ii).

17. (Original) The method of claim 15, wherein each compartment contains a single particle, and each particle contains a single peptoid.

18-20 (Canceled)

21. (Previously presented) The method of claim 13, wherein, in step (iii), each said mixture is contacted with a plurality of distinct cell types.

22-24. (Canceled)

25. (Previously presented) The method of claim 13, wherein in formula I, R^a comprises a lipid moiety, and R^c is selected from $-NH_2$, -NHR, and -NH(C=O)R, where R is lower alkyl.

26. (Original) The method of claim 25, wherein said lipid moiety is a sterol.

27. (Previously presented) The method of claim 13, wherein in formula I, each of R^1 and R^2 is hydrogen.

28. (Previously presented) The method of claim 13, wherein in formula I, at least one R^b includes a group which is cationic at physiologically relevant pH, and at least one R^b is uncharged at physiologically relevant pH.

29. (Previously presented) The method of claim 28, wherein said cationic group is selected from aminoalkyl, ammonium, guanidino, amidino, imidazole, and pyridinium.

30-32 (Canceled)

33. (Previously presented) The method of claim 13, wherein said peptoids having a plurality of different sequences have the general formula II:

$$R^a - (N(R^{b1}) - C(R^1)(R^2)\text{-}C(O)\text{-}N(R^{b2}) - C(R^1)(R^2)\text{-}C(O)\text{-}N(R^{b3}) - C(R^1)(R^2)\text{-}C(O))_n - R^c$$

II

where

R^{b1} is a cationic moiety, R^{b2} is a non-cationic moiety, R^{b3} is a non-cationic moiety at physiologically relevant pH; and

n is an integer selected from 2 to about 16, and wherein

the sequences of individual peptoids in the provided library are unidentified prior to transfection screening.

34. (Previously presented) The method of claim 13, wherein said peptoids comprise at least two different cationic moieties.

35. (Previously presented) The method of claim 13, wherein providing said library comprises synthesizing the library by a mix-and-split protocol.

36. (Previously presented) The method of claim 13, wherein identifying transfecting peptoids comprises determining their sequence.

37. (Previously presented) The method of claim 36, wherein the peptoid sequence is determined by tandem mass spectrometry.

38. (New) A method of identifying peptoids which are effective in transfecting a cell with an oligonucleotide, the method comprising:

(i) providing a plurality of different-sequence peptoids in separated compartments, wherein the sequences of individual peptoids are unidentified;

(ii) forming a peptoid-oligonucleotide mixture in at least one of these compartments, wherein said oligonucleotide is between about 10 and 50 nucleotides in length;

(iii) contacting the mixture with a cell;

(iv) determining the degree of transfection of the cell by the oligonucleotide;

(v) after the degree of transfection is determined, determining the identity of the peptoid.

39. (New) The method of claim 38, wherein the identity of the peptoid is determined if the peptoid was effective in transfecting the cell in (iv).

40. (New) The method of claim 38 wherein the separated compartments are wells on a multi-well plate.